



REPLACEMENT SHEET

SIGNAL 1 atggatgaggcgccgctgcgttgcctgcitllgtagctctctggcttctglocccggg 60
PEPTIDE 1 [M D V A A A A L P A F V A L W L L Y P W 20

61 cctctcctggggtcggcccttggccagttctcagcaggaggctgactlltgalgalggg 120
21 P L L G S] A L G Q F S A [G G C T F D D G 40

A5
HOMOLOGY 121 ccaggggcttgtgactaccaccaggatllatcagatgactlltggagggtccatgacgt 180
REGION 41 P G A C D Y H Q D L Y D D F E W V H V S 60

181 gcgcaggaacctcattacctgcccccgaaatgcctcaagggttccatataggttgaggac 240
61 A Q E P H Y L P P E M P Q G S Y M V V D 80

241 tccatcaatcatgactcctggagaaaaagccagacttcagctgcctaccatgaaggagool 300
81 S S N H D P G E K A R L Q L P T M K E N 100

301 gacaccacatgacttgaattcagttacctgttatatagccagaagggttgaaccttggc 360
101 D T H C I D F S Y L L Y S Q K G L N P G 120

361 accttgaatatcctagttagggtgaataaaggacctcttgcataatccaatlltgaatgla 420
121 T L N I L V R V N K G P L A N P I W N V 140

421 actggattcactggctgctgattggcttcgggctgaactagctgtgagcacctlltggccc 480
141 T G F T G R D W L R A E L A V S T F W P 160

481 aatgaataccaggtaatatlltgaagctgaagctcaggaggaggagaagtggttatattgcc 540
161 N E Y Q V I F E A E V S G G R S G Y I A 180

541 attgatgacatccaatccttgaattatccttgcgataaatctctcattlltccgcctt 600
181 I D D I Q V L S Y] P C D K S P H F L R L 200

FIG.1A

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REPLACEMENT SHEET

601 ggtgatgtggagggtcaatgctgggcagaaatgctacatttcagtgcatgctacagggaga 660
201 G D V E V N A G Q N A T F Q C I A T G R 220

661 gatgctgtgcataaacaagttaaggctgcagagacgcaatggagaaagacatacccgtagcc 720
221 D A V H N K L W L Q R R N G E D I P V A 240

721 cagactaagaacataaatacacagaagatttgctgcctctttcagattgcaagaagtgcac 780
241 Q T K N I N H R R F A A S F R L Q E V T 260

781 aaaactgaccaggatttgtagccgtgcgttaactcagtcagaaacgaggttctggggtttcc 840
261 K T D Q D L Y R C V T Q S E R G S G V S 280

841 oattttgctcaactcattgtgagagaaccacclagacccattgctcctccccagctgctt 900
281 N F A Q L I V R E P P R P I A P P Q L L 300

901 ggtgttgggcctacttacttgctgatccaaactaaatgccaaactctatttggcgatggc 960
301 G V G P T Y L L I Q L N A N S I I G D G 320

961 cccatcatcctgaagaagtagagtatcgaaatgacatcaggatcttggacagaaacccat 1020
321 P I I L K E V E Y R M T S G S W T E T H 340

1021 gcogtcaacgcaccaacatataagttgtggcatttagaccagatcacagaatcagagatc 1080
341 A V N A P T Y K L W H L D P D T E Y E I 360

1081 cgcgtcctgcttaccagacctggcgaagggggaactgggctgccaggaccaccactgatc 1140
361 R V L L T R P G E G G T G L P G P P L I 380

1141 octagaacgaagtgtgcagaaacctatgcggacaccaaaagacttttaagattgctgaaatc 1200
381 T R T K C A E P M R T P K T L K I A E I 400

FIG.1B

REPLACEMENT SHEET

1201 caggcaaggcgcatcgcagtggaactgggagtccttgggctacaacatcactcgttggccac 1260
401 Q A R R I A V D W E S L G Y N I T R C H 420

1261 acittcoacgtcacatctctgctaccattacitccgtggccacatgagagcagggcagac 1320
421 T F N V T I C Y H Y F R G H N E S R A D 440

1321 tgccttggaatggaccccaagccctcagcatgttgtgaacctctgccaccttacaco 1380
441 C L D M D P K A P Q H V V N H L P P Y T 460

1381 aatgtcagcctcaagatgatcctaaccaaccagaggggaaggagagcggaagagaca 1440
461 N V S L K M I L T N P E G R K E S E E T 480

1441 atcatccaaactgatgaagatgtgccgggacctgtgccagtcgaatccctccaaggaaco 1500
481 I I Q T D E D V P G P V P V K S L Q G T 500

1501 tcctttgaaaacaagatcttcctgaactggaaagagccactggaaccgaatggaatttc 1560
501 S F E N K I F L N W K E P L E P N G I I 520

1561 actcagtatgagtgagctatagcagcataagatcatttgaccctgctgttccagtggt 1620
521 T Q Y E V S Y S S I R S F D P A V P V A 540

1621 gggccccacagactgtatcgaatttatggaatagtcacaccatgtatttatgcatt 1680
541 G P P Q T V S N L W N S T H H V F M H L 560

1681 caccctggaaccacctaccagtttttataagagccagcactgtcaaaggctttggacca 1740
561 H P G T T Y Q F F I R A S T V K G F G P 580

1741 gcaacagccatcaatgtgaccocaaatatctcagctccaagcttacctgactatgaagga 1800
581 A T A I N V T T N I S A P S L P D Y E G 600

FIG.1C

REPLACEMENT SHEET

1801	gtlgtgccctctctgaatgaaactgccaccoccatcacaglaactatlgaggcctgcacaa	1860
601	V D A S L N E T A T T I T V L L R P A Q	620
1861	gcccgaaggcctcctatcagtgcttcatcaaatlglltggagcagctaccccacatcga	1920
621	A K G A P I S A Y Q I V V E Q L H P H R	640
1921	acgaagcgtgaagcaggggccatggaaatgctaccagglaccggttccataccagaacgcc	1980
641	T K R E A G A M E C Y Q V P V T Y Q N A	660
1981	ctaagtgggggcgcgccctattcctllgccgcagaactlcccclgggaatcllcccgag	2040
661	L S G G A P Y Y F A A E L P P G N L P E	680
2041	cclgclcccllcccgltgggtgacaaacggacctaataaggtlltggaaacclcccclg	2100
681	P A P F T V G D N R T Y K G F W N P P L	700
2101	gccccccgcaaggatocaaatctatllccaagcgatgagcagltgaggagaaggaaact	2160
701	A P R K G Y N I Y F Q A M S S V E K E T	720
2161	aaaacccaatgtgtacgaattgctacaaaagcagcagcaacagaagaaccagaagtgatc	2220
721	K T Q C V R I A T K A A A T E E P E V I	740
2221	ccagaccggcgaagcagacagacagagtggtgaagaatcgcgggcatcagtgctlggcac	2280
741	P D P A K Q T D R V V K [I A G I S A G I	760
2281	ctagtgttcatccttctcctgctggttgtcatagtaattgtgaaaaagcgaagcttgct	2340
761	L V F I L L L L V V I V I V] K K S K L A	780
2341	aagaagcgcaagatgcaatgggggaacacacgtcaggagatgaccacatggatgaatgct	2400
781	K K R K D A M G N T R Q E M T H M V N A	800

TRANS-
MEMBRANE

FIG.1D

REPLACEMENT SHEET

2401	atggaccgaagttatgctgaccagagcacccctgcatgcagaagaccccccttccctcacc	2460
801	M D R S Y A D Q S T L H A E D P L S L T	820
2461	ttcatggaccaacataacttcagtcgaagattgcccaatgatccacttgigccgactgcc	2520
821	F M D Q H N F S P R L P N D P L V P T A	840
2521	gigttagatgagaaccacagtgccacagcagagtcagtcgtctcctggatgttccctcga	2580
841	V L D E N H S A T A E S S R L L D V P R	860
2581	tacctctgcgaaggagcagagtcaccttalcagacaggacagctgcaccagccatcagg	2640
861	Y L C E G T E S P Y Q T G Q L H P A I R	880
2641	glggccgacttactgcagcacatlaacctcatgaagacalcagacagctatgggttcaaa	2700
881	V A D L L Q H I N L M K T S D S Y G F K	900
2701	gaggaaacagagagcttcttgaaggccagtcagcctcttgggatgtggctaaaaaggat	2760
901	E E Y E S F F E G Q S A S W D V A K K D	920
PTPase DOMAIN I	2761 caaaacagagcaaaagaaccgatacggaaacattatcgcatatgatcactccagagtcac	2820
921	Q N R A K [N R Y G N I I A Y D H S R V I	940
2821	ctgcaacctgtggaagatgaccttcttcagattacattaatgccaaactacatcgacatt	2880
941	L Q P V E D D P S S D Y I N A N Y I D I	960
2881	tggctglacagggatggctaccagagaccaagccactacattgcaactcaaggcccagti	2940
961	W L Y R D G Y Q R P S H Y I A T Q G P V	980
2941	catgaaaccgtatolgatlttttggaggatgggtgiggcaogagcagtcctgtotltgt	3000
981	H E T V Y D F W R M V W Q E Q S A C I V	1000

FIG.1E

REPLACEMENT SHEET

3001	atgggtcactaatttagtgggaagtggccgggtgaaatgctataaattattggcctgatgat	3060
1001	M V T N L V E V G R V K C Y K Y W P D D	1020
3061	actgagggtttatggtagcttcaaagtcacctgcgtagaaatggagccacttgctgogtat	3120
1021	T E V Y G D F K V T C V E M E P L A E Y	1040
3121	gtcgttoggacattcaccttggaaaggagggtatataatgaaatccgtgaagtcaaocag	3180
1041	V V R T F T L E R R G Y N E I R E V K Q	1060
3181	ttccacttcactggctggcctgacctgggtgttccataccacgcaocagggtcctgtca	3240
1061	F H F T G W P D H G V P Y H A T G L L S	1080
3241	tttatccggagagtcgaagctatctaacctcccagtgctgggcccattgtcgtacactgc	3300
1081	F I R R V K L S N P P S A G P I V V H C	1100
3301	ogtgcgtggtgctgggcgcacaggtgttacattgttattgacataatgctggacatggct	3360
1101	S A G A G R T G C Y I V I D I M L D M A	1120
3361	gaaogagaggggtgtggttgacatctacaactgtgtgaaagccttacgatctcggcgcatt	3420
1121	E R E G V V D I Y N C V K A L R S R R I	1140
3421	aatatggtacagocagaggaacagtacattttattcatgatgccattttagaagcctgc	3480
1141	N M V Q T E E Q Y I F I H D A I L E] A C	1160
3481	ttatgtggogaaactgccatccctgtgtgtgaaatgaaagctgcatatttgatgatgt	3540
1161	L C G E T A I P V C E F K A A Y F D M I	1180
3541	cgaatagactctcagactaactcctctcatctcaaogatgaatttcagactctgaattcg	3540
1161	L C G E T A I P V C E F K A A Y F D M I	1180

FIG.1F

	3541	cgaatagacitcagactaacitccitclcatclcaaogotgaaittcagocictgaaitcg	3600
	1181	R I D S Q T N S S H L K D E F Q T L N S	1200
PTPase DOMAIN II	3601	gtccccctcgactacaagctgaagactgcagcalagccitgccitgccaaggaoaccatgac	3660
	1201	V T P R L Q A E D C S I A C L P R [N H D	1220
	3661	aagaaccglitcatggatalgctcccaccitgacagatgicetgccitltitlaattlocaati	3720
	1221	K N R F M D M L P P D R C L P F L I T I	1240
	3721	gatggggagagcaglaactacatcaatgctgctcltalggatagctalaggcagccagca	3780
	1241	D G E S S N Y I N A A L M D S Y R Q P A	1260
	3781	gctlltalcgtcacacaatlacccactlgccaacactlgaagactitclggogatlagto	3840
	1261	A F I V T Q Y P L P N T V K D F W R L V	1280
	3841	tatgattacggatgtacctccatcgtgatgctloaatgaagitggacctgiclcagggtcgc	3900
	1281	Y D Y G C T S I V M L N E V D L S Q G C	1300
	3901	ccacagtlactlgccagaaogaaggaatgctgcgatatggicctalccaagtggaaatglatg	3960
	1301	P Q Y W P E E G M L R Y G P I Q V E C M	1320
	3961	lcttgiltcaatggacttgtatgtgatcaatcgaaitltitagoaalatgcoacctoacgaga	4020
	1321	S C S M D C D V I N R I F R I C N L T R	1340
	4021	ccacaggagggtctatctgatggtaacoacaglitccagtlacctaggctgggtcltclcatcga	4080
	1341	P Q E G Y L M V Q Q F Q Y L G W A S H R	1360
	4081	gaagitgcctggclccaaocgctcgtltitlgaaitlgataclgcaggltggaaaaatggcaa	4140
	1361	E V P G S K R S F L K L I L Q V E K W Q	1380

REPLACEMENT SHEET

4141	gaggaatgtgaagaagggaaggccggacaatcatccactgcttgaatggcggaggcg	4200
1381	E E C E E G E G R T I I H C L N G G G R	1400
4201	ogtggcatgttctgtgccataggcattgttgtggagatggtgaagcggcaaatgtgg	4260
1401	S G M F C A I G I V V E M V K R Q N V V	1420
4261	gatgttttccatgcagtaaaagacgtgaggaaacgaagccaaacatggagggaagccccg	4320
1421	D V F H A V K T L R N S K P N M V E A P	1440
4321	gagcagtatcgtttttgcctatgatgtggcgttagagtacctggagtcctcatog	4374
1441	E Q Y R F C Y D V A L E Y L E] S S *	1458

FIG.1H

REPLACEMENT SHEET

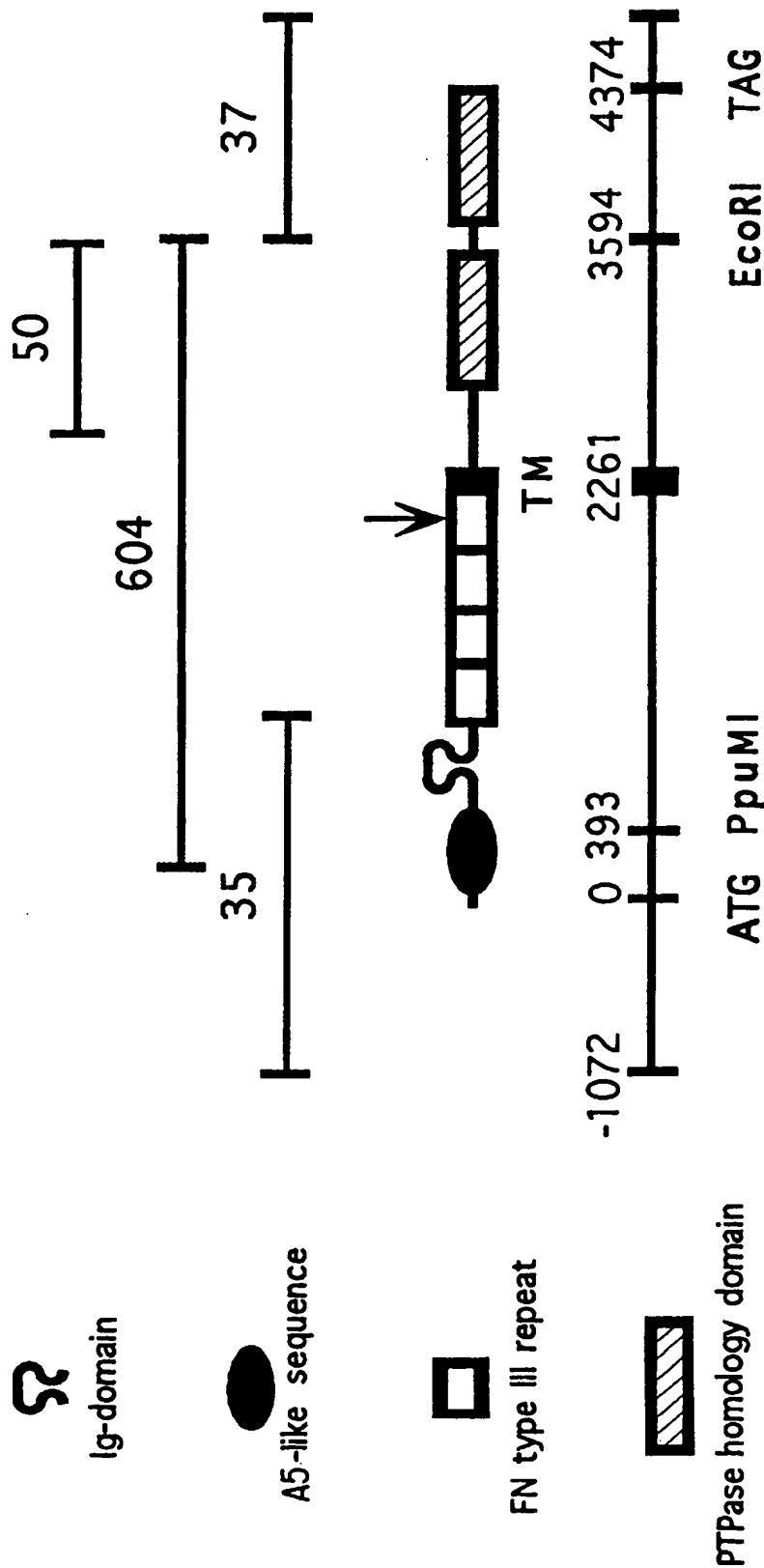


FIG. 2

REPLACEMENT SHEET

1	MDVAAAALPAFVALWLLYPWPPLLGSALGQFSAGGCTFDDGPGACDYHQDL	
51	YDDFEWVHVS AQEPHYLPPEMPQGSYMVVDSSNHDGPEKARLQLPTMKEN	A5
101	DTHCIDFSYLLYSQKGLNPGTLN ILVRV NKGPLANPIWNVTGFTGRDWLR	
151	AELAVSTFWPNEYQVIFEAEVSGCRSGYIAIDDIQVLSYPCDKSPHFLRL	Ig
201	GDVEVNACQNA TFQCIATGRDAVNKKLWLQRRNGEDIPVAQTKNINHRRF	
251	AASFRLQEVTKTDQDL YRCVTQSERGSGVSNFAQLIVREPPRIAPPQLL	FN-III (x4)
301	GVGPTYLLIQLNANSIIGDGP IILKEVEYRMTSCSWTETHAVNAPTYKLW	
351	HLDPDTEYEIRVLLTRPGEGGTGLPGPPLITRTKCAEPMRTPKTLKIAEI	TM
401	QARRIAVDWESLGCYNIITRCHTFNVITICYHYFRGHNESRADCLDMDPKAPQ	
451	HVVNHLPPYTNVSLKMLITNPEGKKESEETIIQTDEDVPGVPVKSLQGT	
501	SFENKIFLNWKEPLEPNGIITQYEVSYSSIRSFDPAPVAGPPQTVSNLW	
551	NSTHHVFMHLHPGCTTYQFFIRASTVKGFGPATAINVTINISAPSLPDYEG	
601	VDASLNETATTITVLLRPAQAKCAPISAYQIVVEQLHPHRTKREAGAMEC	
651	YQVPVTYQNALSGGAPYYFAAELPPGNLPEPAFTVGDNRTYKGFWNPPPL	
701	APRKGCYNIYFQAMSSVEKETKTQCVRIATKAAATEEPEVIPDPAKQTD RV	
751	VK IAGISAGILLVFI LLLVVIIVVKSKLAKKRKDAMGNTREQEMTHMVNA	
801	MDRSYADQSTLHAE DPLSLTFMDQHNFSPRLPNDPLVPTAVLDENHSATA	
851	ESSRLLDVPRYLC EGTESPYQTGQLHPAIRVADLLQHINLMKTSYGFK	
901	EEYESFFEGQSASWDVAKKDQNRAKNRYGNITAYDHSRVLQPVEDDPSS	PTP-1
951	DYINANYIDIWL YRDGYQRPSHYIATQGPVHETVYDFWRMVWQEQSACIV	
1001	MVTNLVEVGRVKCYKYWPDDTEVYCDFKVTCEMEPLAEYVVRTFTLERR	
1051	GYNEIREVKQFHFTGWP DHGVPYHATGLLSFIRRVKLSNPPSAGPIVVHC	
1101	SACAGRTGCYIVIDIML DMAEREGVVDIYNCVKALRSRRINMVQTEEQYI	
1151	FIHDAILEACLCGETAIPVCEFKAAFFDMIRIDSQTNSSH LKDEFQTLNS	
1201	VTPLRQAEDCSIA CLPRNHDKNRFRMDMLPPDRCLPFLITIDGESSNYINA	PTP-2
1251	ALMDSYRQPAAFIVTQYPLPNTVKDFWRLVYDYGCTSI VMLNEVDLSQGC	
1301	PQYWPEEGMLRYCPIQVECMSCSMDCDVINRIFRICNLTRPQECYLMVQQ	
1351	FQYLGWASHREVPGSKRSFLKLI LQVEKWKQEECEEGEGRITIHCLNGGGR	
1401	SCMFCAIGIVVEMVKRQNVVDVFHAVKTLRNSKPNMVEAPEQYRFCYDVA	
1451	LEYLESS*	

FIG.3

REPLACEMENT SHEET

I (296) P PQL L GVGPTYLLIQLNANS I IGDGPIILKEVE Y RMTSGSWTEHAVNAPTYKLWHLDPOTE. YEIRVLL T R PG EG G TGLPGPPLITRT
II (392) P .KT L KIAEIQA..RRIAYD W ESLGYNITRCHT F NVTICHYFRGHNESRADCLDADPKA...PQRVNH L P PY TN V SLKMIL..INPEG
III (493) P VKS L QGTSFE...NKIFLN W KEPLPNCIITQ Y EVSYSSIRSFDPANPVAGPPQTVSNLWNSTHVFMH L H PG TT Y QFFIRASTVKGF
IV (596) P DYE G VDASLNETATTITVL L RPAQAKGAPISA Y QIWEQLHPHRTKR.EAGAMECYQV....PVTYQNA L S GG AP Y YFAAELPPGNLP
FBN-III(7) P PTN L HLEANPDT.GVLTVS W ERSTTPD...ITG Y RITITPTNGQGNLSLEEWHADQ.....SSCTFDN L S PG LE Y NVSVY...TWKDD

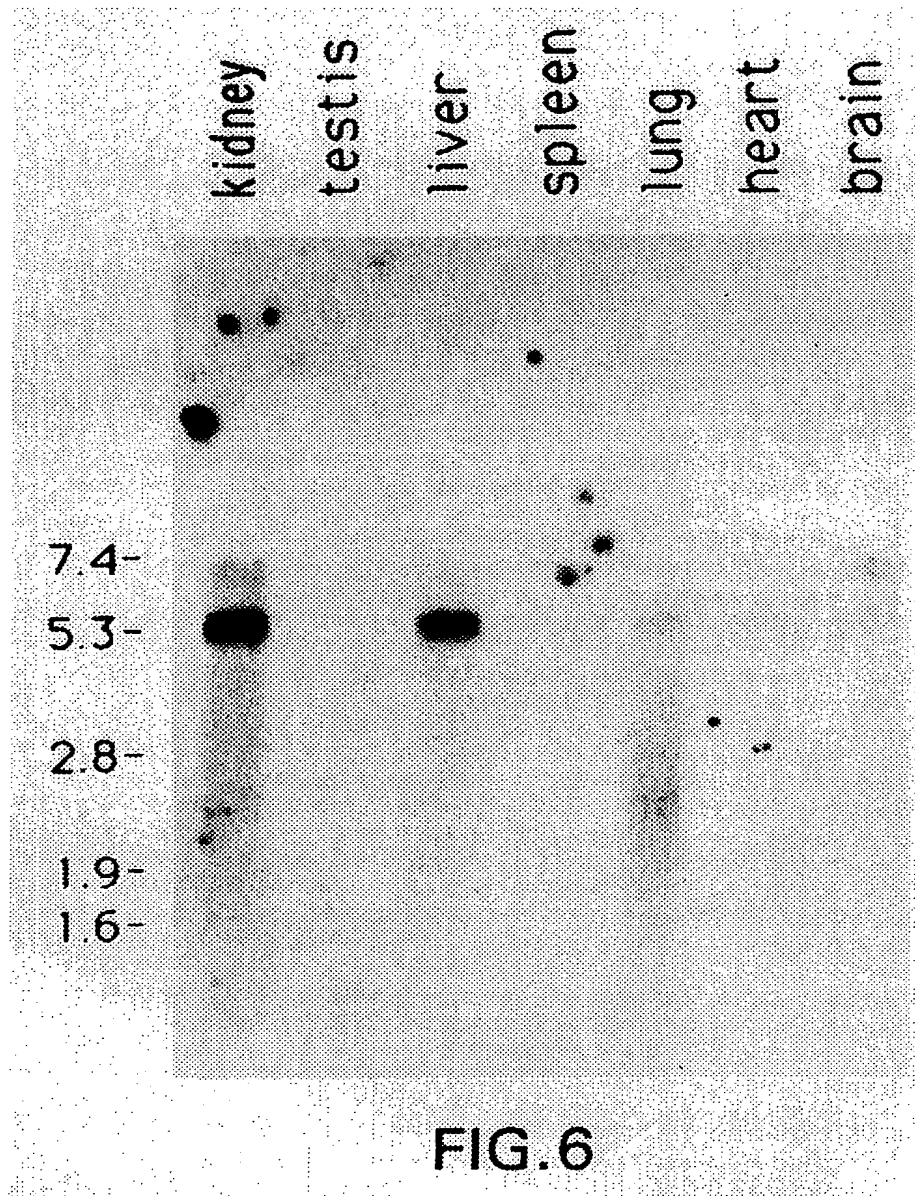
FIG.4

PTP-κ (34) GGCTFDDGPGACDYHQDL YDDFEWVHVSAGE .PHYLPPMPQGSYMWVDSNHDGPEKARLQLPTMKEN.DTHCIDFSYLLYSOK
PTP-μ (26) GGCLFDEPYSTCGYSQADEDFNWEQVNTLTKPT .SDPMPSGSFMILVNTSGKPEGQRAHLLLPQLKEN.DTHCIDFHYFVSSKS
A5 (651) CKFCNGSOKTVCNWHQHDISSDLKWAVLNSKTGP..VQDHTGDGNF IYSEADERHEGRAARLMSPVSSSRSAHCLTFWYIM...D
Consensus C—D—D—W—N—T—P—G—F—EG—ARL—P—HC—F—Y—

PTP-κ GLNPGTLNILVRVN.KGPLANP IWNVTGFTGROWLRAELAVSTFWPNEYQVIFEAVSGGRSGYIAIDDIQVLSY
PTP-μ NAAPGLLNVYKVN.NGPLGNP IWNISGDPTRTHRAELAISTFWPNFYQVIFEV .VTSCHQGYLAIDEVKVLGH
A5 GSHVGTLSIKLYEMEEDFQTLWTVSGNCGDQWKEARVVLHKTMKQ.YQVIVEGTGKGSAGGIAVDDIIIANH
Consensus G—GTL—I—K—W—VSC—G—W—A—YQVI—E—V—G—G—A—DDI—H

FIG.5

REPLACEMENT SHEET



REPLACEMENT SHEET

Transfected:	-	-	-	+	+	+
Antibody:	pre	α - κ	α - κ	pre	α - κ	α - κ
Peptide:	-	-	+	-	-	+

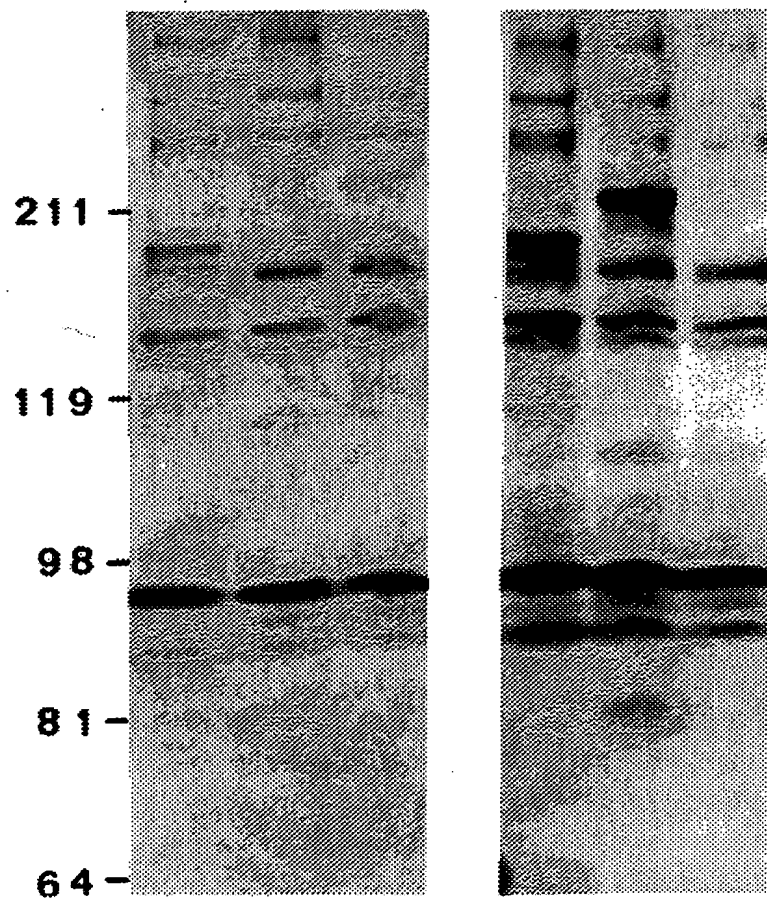


FIG. 7

REPLACEMENT SHEET

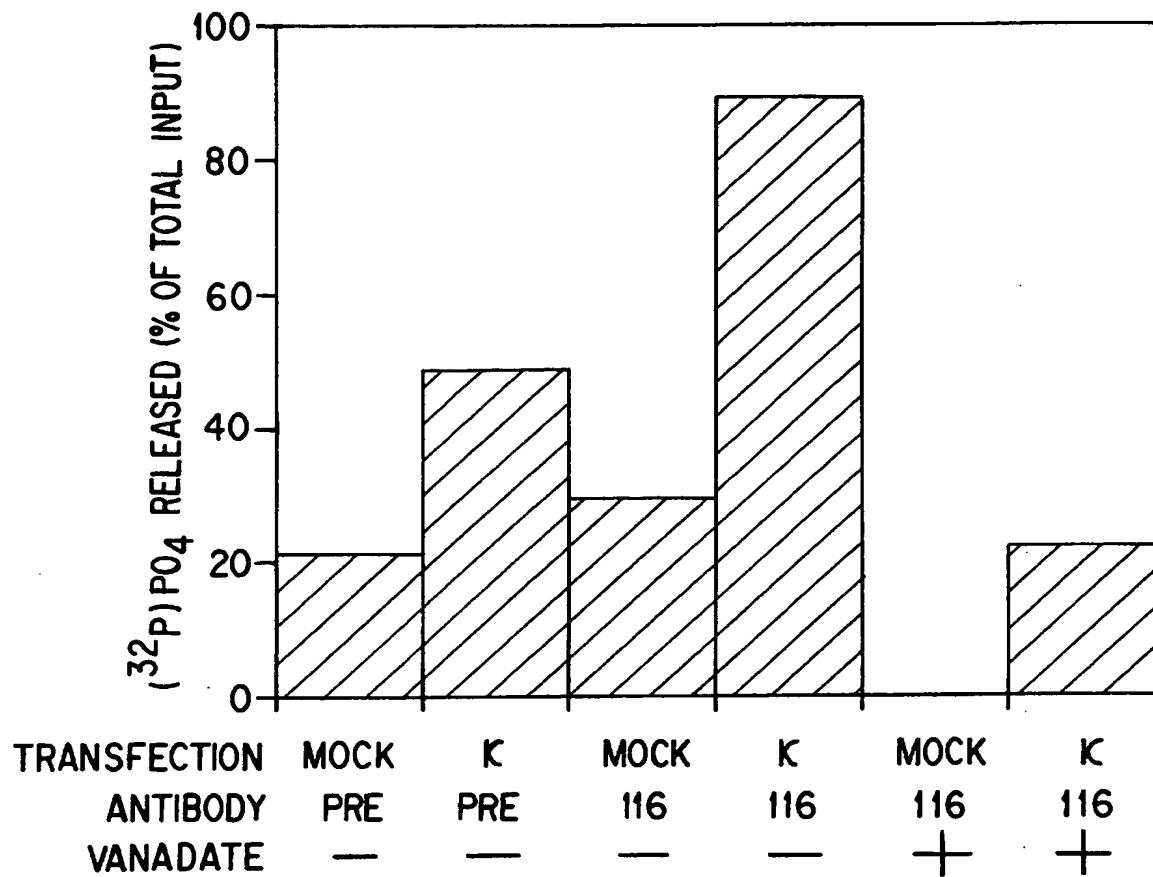


FIG. 8

REPLACEMENT SHEET

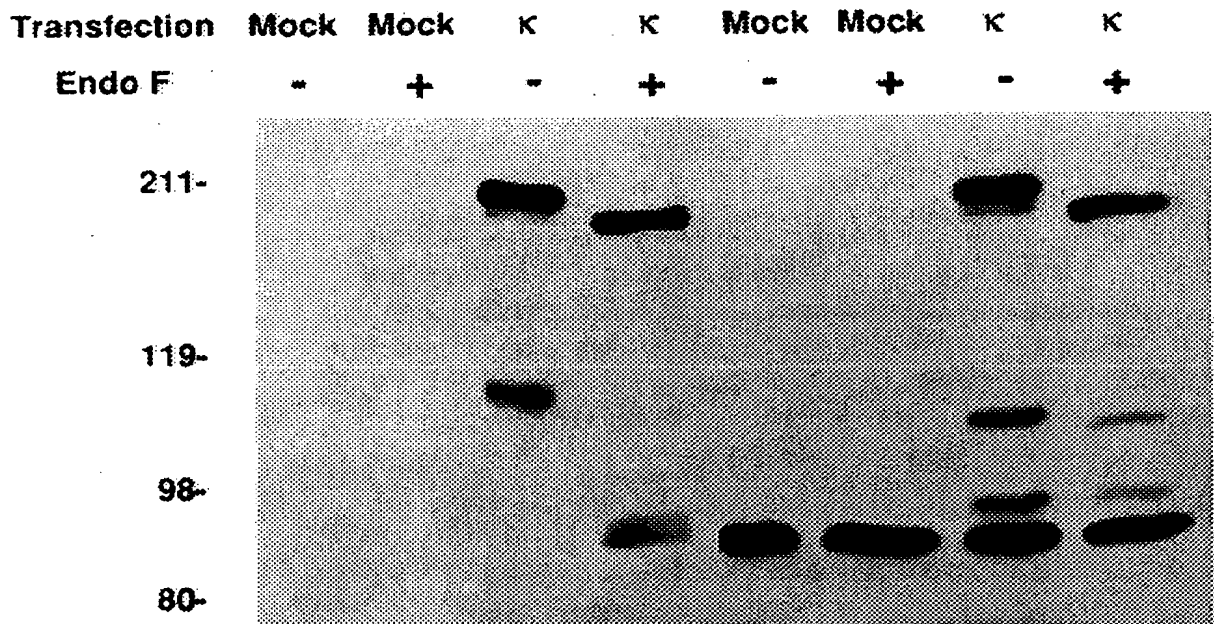


FIG. 9

REPLACEMENT SHEET

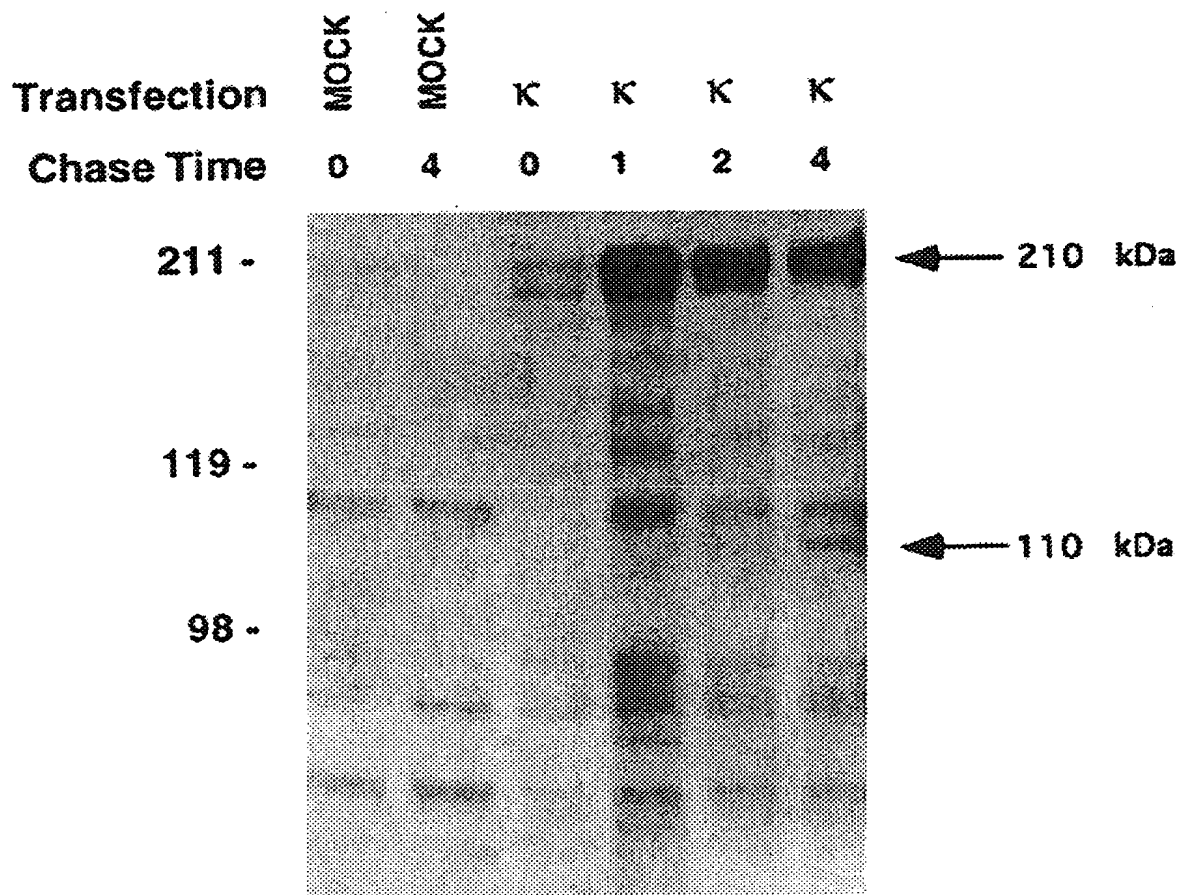


FIG. 10

REPLACEMENT SHEET

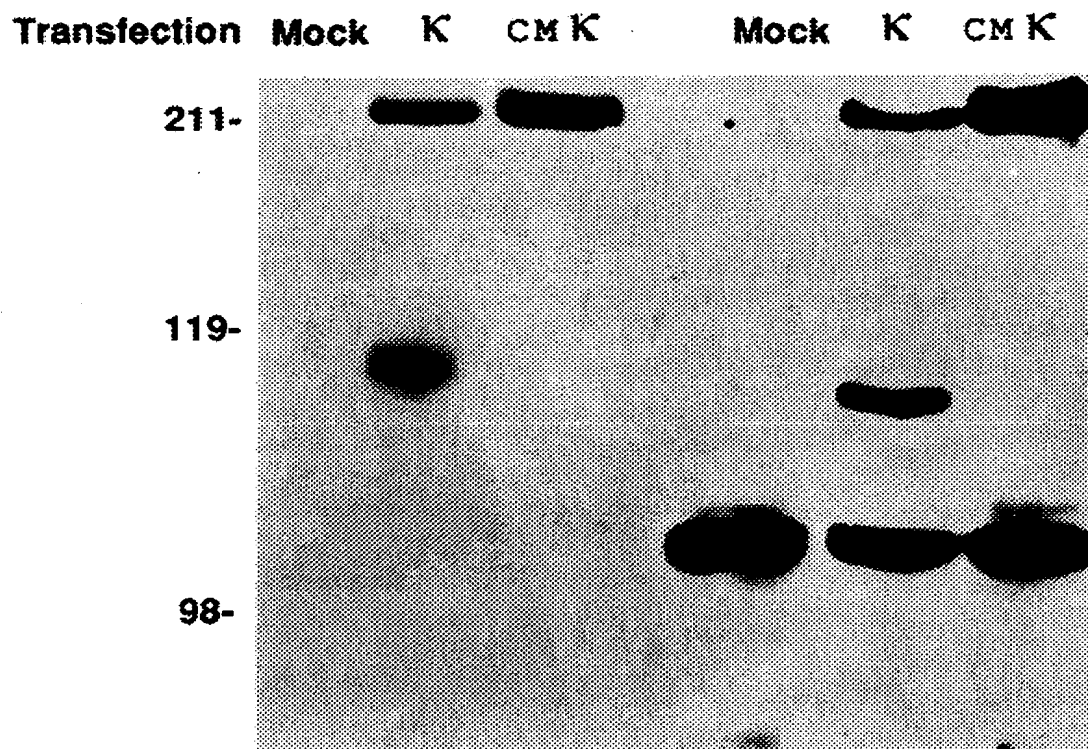


FIG. 11

REPLACEMENT SHEET

Transfection Mock K K
IP 116 116 Total
 lysate

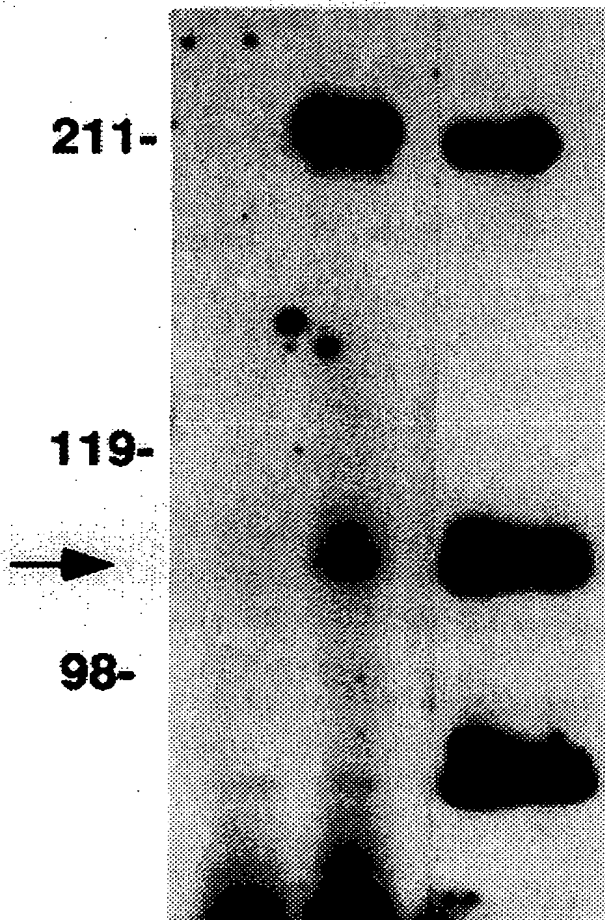


FIG. 12

REPLACEMENT SHEET

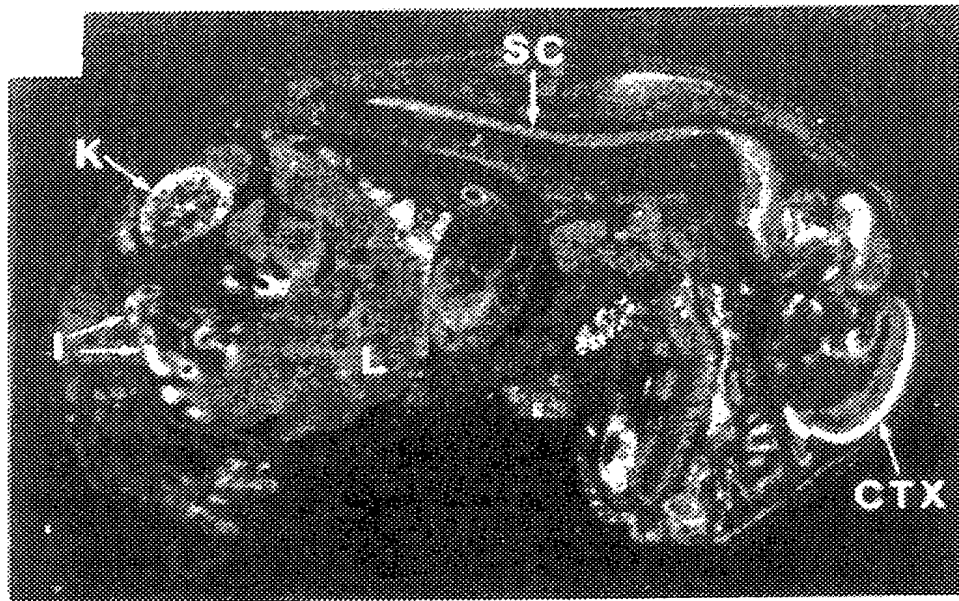


FIG. 13A

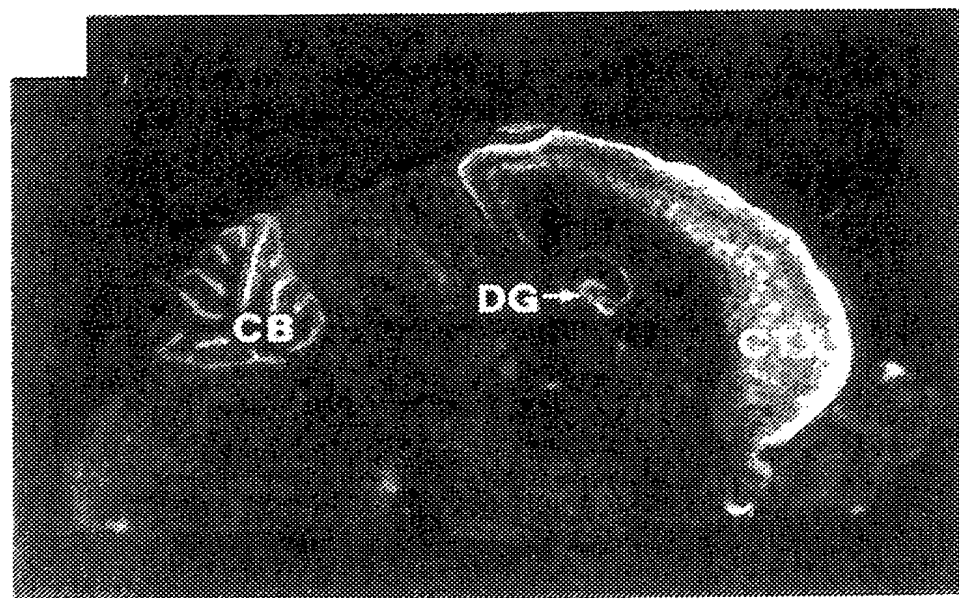


FIG. 13B

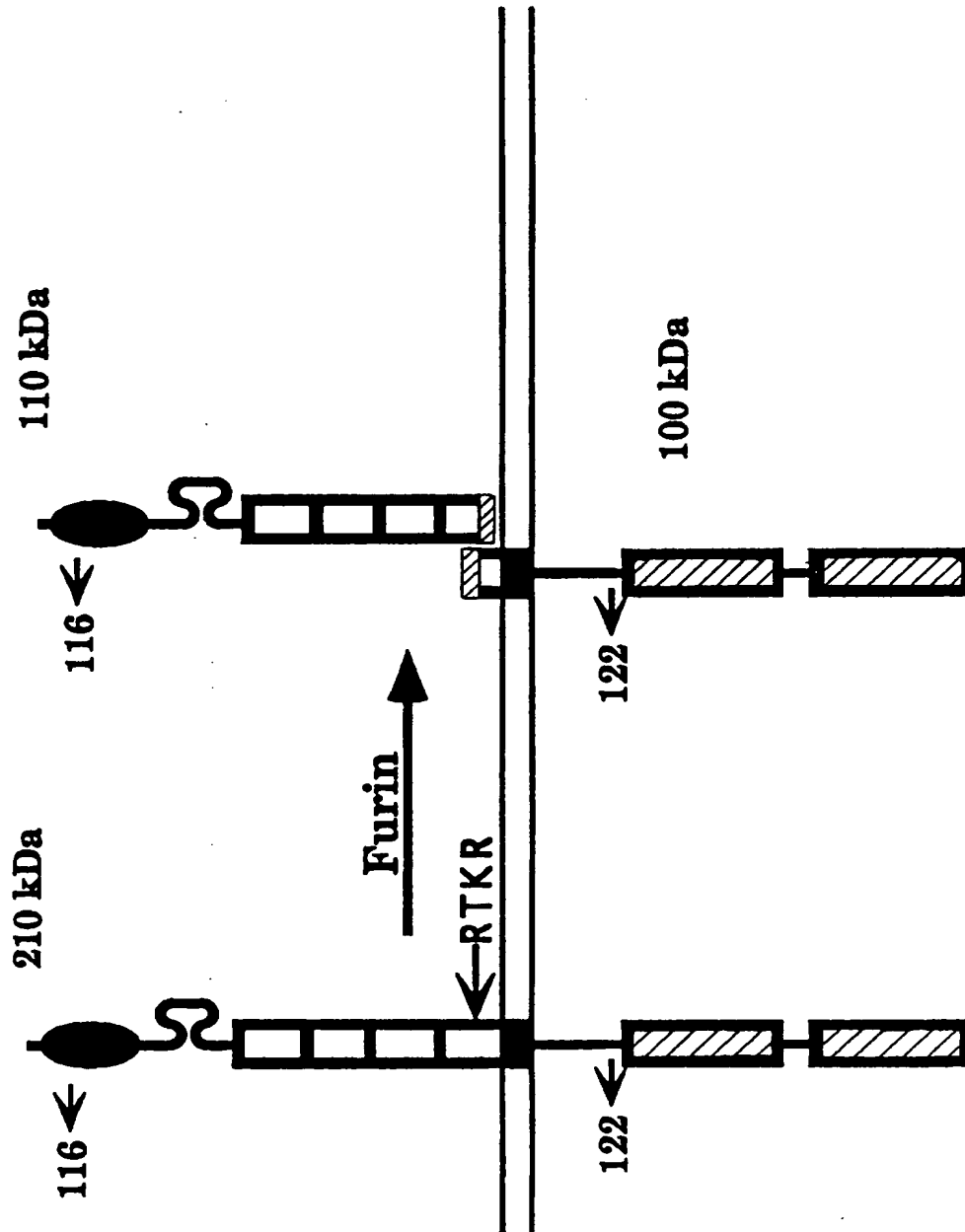


FIG. 14

REPLACEMENT SHEET

1 ATGGATACGACTGCGGGGGGGGGCTGCCTGCTTTTGTGGCGCTCTTGCTCCTCTCCTTGGCCTCTCCTGGGATCGGC 80
1 M D T T A A A A L P A F V A L L L L S P W P L L G S A 27

81 CCAAGGCCAGTTCTCCGAGGTGGCTGTACTTTTGATGATGGTCCAGGGGCTGTGATTACCACCAGGATCTGTATGATG 160
27 Q G Q F S A G G C T F D D G P G A C D Y H Q D L Y D D 53

161 ACTTTGAATGGGTGCATGTTAGTGCTCAAGAGCCTCATTATCTACCAACCGAGATGCCCCAAGGTTCTATATGATAGTG 240
54 F E W V H V S A Q E P H Y L P P E M P Q G S Y M I V 80

241 GACTCTTCAGATCAGACCTGGAGAAAAAGCCAGACTTCAGCTGCCTACAATGAAGGAGAAGCACTCACTGCATTGA 320
81 D S S D H D P G E K A R L Q L P T M K E N D T H C I D 107

321 TTTCAGTTACCTATTATATAGCCAGAAAGGACTGAATCCTGGCACTTTGAACATATTAGTTAGGGTGAATAAAGGACCTC 400
107 F S Y L L Y S Q K G L N P G T L N I L V R V N K G P L 133

401 TTGCCAATCCAATTTGGAATGTGACTGGATTACGGGTAGAGATTGGCTTCGGGCTGAGCTAGCAGTGAGCACCTTTTGG 480
134 A N P I W N V T G F T G R D W L R A E L A V S T F W 160

481 CCCAATGAATATCAGGTAATATTGAAGCTGAAGTCTCAGGAGGGAGAAGTGGTTATATTGCCATTGATGACATCCAAGT 560
161 P N E Y Q V I F E A E V S G G R S G Y I A I D D I Q V 187

561 ACTGAGTTATCCTTGTGATAAATCTCCTCATTTCTCCGCTAGGGGATGTAGAGGTGAATGCAGGGCAAAACGCTACAT 640
187 L S Y P C D K S P H F L R L G D V E V N A G Q N A T F 213

641 TTCAGTGCATTGCCACAGGGAGAGATGCTGTGCATAACAAGTTATGGCTCCAGAGACGAAATGGAGAAGATATACCAGTA 720
214 Q C I A T G R D A V H N K L W L Q R R N G E D I P V 240

721 GCCCAGACTAAGAACATCAATCATAGAAGGTTTGGCGCTTCCTTCAGATTGCAAGAAGTGACAAAACTGACCAGGATTT 800
241 A Q T K N I N H R R F A A S F R L Q E V T K T D Q D L 267

801 GTATCGCTGTGTAACCTCAGTCAGAACGAGTTCCGGTGTGTCCAATTTTGCTCAACTTATTGTGAGAGAACCGCCAAGAC 880
267 Y R C V T Q S E R G S G V S N F A Q L I V R E P P R P 293

881 CCATTGCTCCTCCTCAGCTTCTTGGTGTGGGCCTACATATTTGCTGATCCAATAAATGCCAACTCGATCATTGGCGAT 960
294 I A P P Q L L G V G P T Y L L I Q L N A N S I I G D 320

961 GGTCTATCATCCTGAAAGAAGTAGAGTACCGAATGACATCAGGATCCTGGACAGAAACCATGCAGTCAATGCTCCAAC 1040
321 G P I I L K E V E Y R M T S G S W T E T H A V N A P T 347

FIG.15A

REPLACEMENT SHEET

1041 TTACAAATTATGGCATTAGATCCAGATACCGAATATGAGATCCGAGTTCTACTTACAAGACCTGGTGAAGGTGGAACGG 1120
347 Y K L W H L D P D T E Y E I R V L L T R P G E G G T G 373

1121 GGCTCCCAGGACCTCCACTAATCACCAGAACAAAATGTGCAGAACCTATGAGAACCCAAAGACATTAAAGATTGCTGAA 1200
374 L P G P P L I T R T K C A E P M R T P K T L K I A E 400

1201 ATACAGGCAAGACCGATTGCTGTGGACTGGGAATCCTTGGGTACAACATTACGGTTGCCACACTTTTAATGTCACTAT 1280
401 I Q A R R I A V D W E S L G Y N I T R C H T F N V T I 427

1281 CTGCTACCATTACTTCGGTGCACAACGAGAGCAAGGCAGACTGTTTGACATGGACCCAAAGCCCTCAGCATGTTG 1360
427 C Y H Y F R G H N E S K A D C L D M D P K A P Q H V V 453

1361 TGAACCATCTGCCACCTTATACAAATGTCAGCCTCAAGATGATCCTAACCAATCCAGAGGGAAGGAAGCAGAGTGAAGAG 1440
454 N H L P P Y T N V S L K M I L T N P E G R K E S E E 480

1441 ACAATTATTCAAACGTATGAAGATGTGCCTGGTCCGTACCAGTAAAATCTCTTCAAGGAACATCCTTTGAAAATAAGAT 1520
481 T I I Q T D E D V P G P V P V K S L Q G T S F E N K I 507

1521 CTTCTTGAAGTGAAGAAGCCTTTGGATCCAAATGGAATCATCACTCAATATGAGATCAGCTATAGCAGTATAAGATCAT 1600
507 F L N W K E P L D P N G I I T Q Y E I S Y S S I R S F 533

1601 TTGATCCTGCAGTCCAGTGGCTGGACCTCCCGAGCTGTATCAAATTTATGGAACAGTACACACCATGTCTTTATGCAT 1680
534 D P A V P V A G P P Q T V S N L W N S T H H V F M H 560

1681 CTCCACCTGGAACACGTACCAGTTTTTCATAAGAGCCAGCAGGTCAAAGGCTTTGGTCCAGCCACAGCCATCAATGT 1760
561 L H P G T T Y Q F F I R A S T V K G F G P A T A I N V 567

1761 CACCACCAATATCTCAGCTCCAACCTTTACCTGACTATGAAGGAGTTGATGCCTCTCTCAATGAAACTGCCACCACAATAA 1840
587 T T N I S A P T L P D Y E G V D A S L N E T A T T I T 613

1841 CTGTATTGTTGAGACCAGCACAAGCCAAAGGTGCTCCTATCAGTGCTTATCAGATTGTTGTGGAAGAACTGCAACCCACAC 1920
614 V L L R P A Q A K G A P I S A Y Q I V V E E L H P H 640

1921 CGAACCAAGAGAGAAGCCGGAGCCATGGAATGCTACCAGTTCTGTGCATACCAAAATGCCATGAGTGGGGTGCACC 2000
641 R T K R E A G A M E C Y Q V P V T Y Q N A M S G G A P 667

2001 GTATTACTTTGCTGCAGAACTACCCCGGAAACCTACCTGAGCCTGCCCGTTCACTGTGGGTGACAATCGGACCTACC 2080
667 Y Y F A A E L P P G N L P E P A P F T V G D N R T Y Q 693

2081 AAGGCTTTTGAACCTCCTTTGGCTCCGCGCAAAGGATACAACATCTATTTCCAGCGATGAGCAGTGTGAGAAGGAA 2160
694 G F W N P P L A P R K G Y N I Y F Q A M S S V E K E 720

FIG.15B

REPLACEMENT SHEET

2161 ACTAAAACCCAGTGGTAACGATTGCTACAAAAGCAGCAACAGAAGAACCAGAAGTGATCCCAGATCCGCCAAGCAGAC 2240
721 T K T Q C V R I A T K A A T E E P E V I P D P A K Q T 747

2241 AGACAGAGTGGTGAATAAGCAGGAATTAGTGCTGGAATTTGGTGTTTCATCCTCCTTCTCCTAGTTGTCATATTAATTG 2320
747 D R V V K I A G I S A G I L V F I L L L L V V I L I V 773

2321 TAAAAAGAGCAAACCTTGCTAAAAACGCAAGATGCCATGGGAATACCCGGCAGGAGATGACTCAGATGGTGAATGCA 2400
774 K K S K L A K K R K D A M G N T R Q E M T H M V N A 800

2401 ATGGATCGAAGTTATGCTGATCAGAGCACTCTGCATGCAGAAGATCCTCTTTCCATCACCTTCATGGACCAACATAACTT 2480
801 M D R S Y A D Q S T L H A E D P L S I T F M D Q H N F 827

2481 TAGTCCAAGATATGAGAACCACAGTGTACAGCAGAGTCCAGTGCCTTCTAGACGTACCTCGCTACCTCTGTGAGGGGA 2560
827 S P R Y E N H S A T A E S S R L L D V P R Y L C E G T 853

2561 CGGAATCCCCTTACCAGACAGGACAGCTGCATCCAGCCATCAGGTAGCTGATTTACTGCAGCACATTAATCTCATGAAG 2640
854 E S P Y Q T G Q L H P A I R V A D L L Q H I N L M K 880

2641 ACATCAGACAGCTATGGGTTCAAAGAGGAATATGAGAGCTTTTTTGAAGCAGCTCAGCATCTTGGGATGTAGCTAAAAA 2720
881 T S D S Y G F K E E Y E S F F E G Q S A S W D V A K K 907

2721 AGATCAAAATAGAGCAAAAACCGATATGGAACATTATAGCATATGATCACTCCAGAGTGATTTTGCAACCCGTAGAGG 2800
907 D Q N R A K N R Y G N I I A Y D H S R V I L Q P V E D 933

2801 ATGATCCTTCTCAGATTATATTAATGCCAACTATATTGATGGCTACCAGAGACCAAGTCATTACATTGCAACCCAAGGT 2880
934 D P S S D Y I N A N Y I D G Y Q R P S H Y I A T Q G 960

2881 CCGTTCATGAAACAGTGTATGATTTCTGGAGGATGATTTGGCAAGAACAATCTGCTTGCAATTGTGATGGTTACAAATTT 2960
961 P V H E T V Y D F W R M I W Q E Q S A C I V M V T N L 987

2961 AGTTGAGGTTGGCCGGTTAAATGCTATAAAATATTGGCCTGATGATACTGAAGTTTATGGTGACTTCAAAGTAACGTGTG 3040
987 V E V G R V K C Y K Y W P D D T E V Y G D F K V T C V 1013

3041 TAGAAATGGAACCACTTGCTGAATATGTAGTTAGGACATTACCCTGGAAAGGAGGGGTACAATGAAATCCGTGAAGTT 3120
1014 E M E P L A E Y V V R T F T L E R R G Y N E I R E V 1040

3121 AAACAGTTCCATTTACGGGCTGGCCTGACCATGGAGTGCCCTACCATGCTACAGGGCTGCTTTCTTTATCCGGCGAGT 3200
1041 K Q F H F T G W P D H G V P Y H A T G L L S F I R R V 1067

FIG.15C

REPLACEMENT SHEET

3201 CAAGTTATCAAACCTCCAGTGCTGGCCCATCGTTGTACATTGCAGTGCTGGTGCTGGACGAAGCTGGCTGCTACATTG 3280
1067 K L S N P P S A G P I V V H C S A G A G R T G C Y I V 1093

3281 TGATTGACATCATGCTAGACATGGCTGAAAGAGAGGGTGTGTGTGATTTACAATTGTGTCAAAGCCTTAAGATCTCGG 3360
1094 I D I M L D M A E R E G V V D I Y N C V K A L R S R 1120

3361 CGTATTAATATGGTCCAGACAGAGAACAGTACATTTTTATTTCATGATGCCATTTTGAAGCCTGCTTATGTGGAGAAAC 3440
1121 R I N M V Q T E E Q Y I F I H D A I L E A C L C G E T 1147

3441 TGCCATACCTGCTCTGTAATTTAAAGCTGCATATTTTGATATGATTAGAATAGACTCCAGACTAACTTTCACATCTCA 3520
1147 A I F V C E F K A A Y F D M I R I D S Q T N S S H L K 1173

3521 AGGATGAATTTGAGACTCTGAATTCAGTCACCCCTCGACTACAAGCTGAAGACTGCAGTATAGCGTGCCGCGCAAGGAAC 3600
1174 D E F Q T L N S V T P R L Q A E D C S I A C L P R N 1200

3601 CATGACAAGAACCGTTTCATGGACATGCTGCCACCTGACAGATGCTGCCTTTTTAATTACAATTGATGGGAGAGCAG 3680
1201 H D K N R F M D M L P P D R C L P F L I T I D G E S S 1227

3681 TAACTACATCAATGCTGCTCTTATGGACAGCTACAGGCAACCAGCTGCTTTCATGTCACACAATACCCCTGCCAAACA 3760
1227 N Y I N A A L M D S Y R Q P A A F I V T Q Y P L P N T 1253

3761 CTGTAAAGACTTCTGGAGATTAGTGTATGATTATGGCTGTACCTCCATTGTGATGTTAAAGCAAGTCGACTGTCCCAG 3840
1254 V K D F W R L V Y D Y G C T S I V M L N E V D L S Q 1280

3841 GGCTGCCCTCAGTACTGGCCAGAGGAAGGATGCTACGATATGGCCCATCCAAGTGAATGTATGCTTGTTCATCGA 3920
1281 G C P Q Y W P E E G M L R Y G P I Q V E C M S C S M D 1307

3921 CTGTGATGTGATCAACCGGATTTTTAGGATATGCAATCTAACAAGACCACAGGAAGTTATCTGATGGTGCAACAGTTTC 4000
1307 C D V I N R I F R I C N L T R P Q E G Y L M V Q Q F Q 1333

4001 AGTACCTAGGATGGCTTCTCATCGAGAAGTGCTGGATCCAAAAGGTATTCTTGAAACTGATACTTCAGGTGGAAGAG 4080
1334 Y L G W A S H R E V P G S K R S F L K L I L Q V E K 1360

4081 TGGCAGGAGGAATGCGAGGAAGGGAAGGCCGACGATTATCCACTGCCATAATGGTGGCGGGCAAGTGGCATGTTCTG 4160
1361 W Q E E C E E G E G R T I I H C L N G G G R S G M F C 1387

4161 TGCTATAGGCATCGTTGTTGAAATGGTGAACCGCAAAATGTTGTCGATGTTTCCATGCAGTAAAGACACTGAGGAACA 4240
1387 A I G I V V E M V K R Q N V V D V F H A V K T L R N S 1413

FIG.15D

REPLACEMENT SHEET

4241 GCAAGCCAAACATGGTGAAGCCCCGGAGCAATACCGTTTCTGCTATGATGTAGCTTTGGAGTACCTGGAATCATCTTAG 4320
1414 K P N M V E A P E Q Y R F C Y D V A L E Y L E S S * 1439
SEQ. ID NO: 2
4321 TTGGGTGAGACTCTTTAAAGTGCATCCATGAAGAAACCTGTCCATCTATTGAGCCAGCAGCTGTGTACCTGTTACACTT 4400
4401 GTGCAGAAAGATTTTAATGTGGCGGTGGGAGACTTTTACATTGAGAGGTAAAAGTATTTTTTTATGAAGTTGTGTAT 4480
4481 CTTAATAAAAAGAACTGAATTAGTTTTTATTACTATATTAAAGCATCAACATTTTCATGCCACATAAAATTATATTTAATA 4560
4561 AGAACCAGATTGAAATGAGAACGTATTGGTGTGTACAGTGAACATGCCACCTTTTCCATGGTTTCAGGTAGTGCAGC 4640
4641 TACCACATGTT 4651

SEQ. ID NO: 4

FIG.15E

REPLACEMENT SHEET

MCP7	MDTTAAALPAPVALLLLSPWLLGSACQPSAGCGTFDDGACDYHQDL YDDFEWHVSAQEPHYLPPEMPQGSYMIIV	80
hrRTP μ	-MR LGTC - TL G -----TAAGET - L EPIST G S SEG N EQ NTLTKPTSD W S L L	71
MCP7	DSSDHPCEKARLQLPTMKENDTHCIDFSYLLYSCKGLNPGTLNLLVRNKGPLANPIMNVTCFTGRDWLRAELAVSTFW	160
hrRTP μ	NA GRPE QR H L QL H FVS KSNSP L VY K N G IS DPT T N I	151
MCP7	PNEYQVIFAEVSGRSGYIAIDDIOVLSPCKSPHFLRLGDVEVNAGQNAIFQC IATGRDAVHNKLWLQRRNGEDIPV	240
hrRTP μ	F V-IITS HQ L EVK CH TRT ICN P S I TVAGDR GIDVR A L	230
MCP7	AQTKNINHRRFAASFRLQEVTKTDODLYRCVTSQERSCVSNFAQLIVREPRPIAPPQLLGCGPTYLLIQLNANSIIGD	320
hrRTP μ	KEI VTSS I NVVNT R AGK MIRT G V I Y E V K V AS A W N	310
MCP7	GPTILLKEVEYRMTCGSWTETHAVNAPTYKLWHLDPDTEYEIRVLLIRPCEGGTGLPGPPLITRTKCAEPMRTPKTLKIAE	400
hrRTP μ	VAR CTA NDRQP DSTS IG S S A R D G RK EW	390
MCP7	IQARRIADWESLGYNIITRCHTFNWTICYHYFRGNE--SKADCLMDPKAPQHVNHLPPTYNVSLKMLITNPEGRKES	478
hrRTP μ	VKS Q TIR PF V SY L VH C QV GQ QVREEVSW TENSHTITN S V L M	470
MCP7	EETIIQIDEDVPGVPVKSQGSFENKIFLNWKEPLDPNGIITQYEISYSSIRSEDPAPVAGPPQTVSNLWNSTHWF	558
hrRTP μ	Q L V L A TE I ST E Q R TQTY V L T KAVS EIDLNQSGR K G E FL	550
MCP7	MHLPGTITYOFFIRASTVKGFGPATAINVTNISAPTLPDYECVDASLNETAITITVLLRPAQAKGAPISAYQIVVEELH	638
hrRTP μ	PG Y ST A PATNQF K SM A -LETP Q DN V M K HSR V V ER	629
MCP7	PHRTKREAGAMECYQVPVTVQNANSGCAPYFAELPPGNLPEPAPFTVGDNRTYQGFNPPPLAPRKGYNIYFQAMSSVE	718
hrRTP μ	R KTTEILK P IHF SLLNSQ F ADS QAAQ I K N Y T L Y S R A RAN	709

FIG.16A

REPLACEMENT SHEET

MCP7	KETKTCVRIATKAATEEPEVIPDPAKQTDKWKIAGISAGILVFILLLLVILIVKSKLAKKRDAMGNITROEMTHMV	798
hRPTP μ	G ID QV G A-T KPV E E HT VI L VIIF G V VM R ET SS V	788

MCP7	NAMORSYADQSTLHAEDPLSITFMDOHNFSPRY-----ENHSATAESSRLLDVPRY-LCE	852
hRPTP μ	S K E G -NDEAF -- T LING SVSPSSFTMKNTILSTSPKSYYPD T TMASDT S VQSH T KKR	865
MCP7	GIESPYQTGQLHPAIRVADLLQHIINLMKTSDSYGFKEEYESFFEGQSASNDVAKKQDNRAKNRYGNI IAYDHSRVILQPV	932
hRPTP μ	PADV TQ CAEG P S E M R TI	945
MCP7	EDDPSSDYINANYIDGYQRPESHYIATQGPVHE TVYDFWRMIWDEQSAC IVMVTNLVEGRVKCYKYMPDDTEVYGD FKV T	1012
hRPTP μ	G TN G H N MQ I V H NT S I C I K I	1025
MCP7	CVEMPLAEYVWRFTLERRGYNE IREVKQHF TQMPDHGVPYHATGLLSFIRRVKLSNPPSAGPIVWHCSAGAGRTGCY	1092
hRPTP μ	LI T L I AV K VH IR G V Q SKS L F	1105
MCP7	IVIDIMDMAEREGVDIYNCVKALRSRRINMWQTEEQYIF IHDAILLEACLCGETAIPVCFEKAAYFDMIRIDSQINSSH	1172
hRPTP μ	RE V V V D SV ASQVRS L Y NKL P Q	1185
MCP7	LKDEFQTLNSVTPRLQAEDCS IACLPRNHDKNRFMDMLPPDRCLPFLITIDGESSNY INAAIMDSYRPAAF IVTQYPLP	1252
hRPTP μ	I E R M T RV L E C I K S H	1265
MCP7	NTVKDFWRLVYDYGCTSI VMLNEVDLSQCGCPQYMFEEGMLRYGPIQVECMSCSDDCDVINRIFRICNL TRPOEGYLMVQQ	1332
hRPTP μ	L H V D PA L N VH H FV ADLEE I S Y AA D R	1345
MCP7	FQYLGWASHREVPCKRSF LKLILOVEKWDECECEGEGRIT I IHLNGGGRSGMFC AIG I VEWKRONVVDVFHVKTLR	1412
hRPTP μ	F PMY DT V R D YNG P W T S C LRH RT	1425
MCP7	NSKPNMEAPEQYRF CYDVALEYLESS*	1439
hRPTP μ	N DLLD K E N G*	1452

FIG.16B

REPLACEMENT SHEET

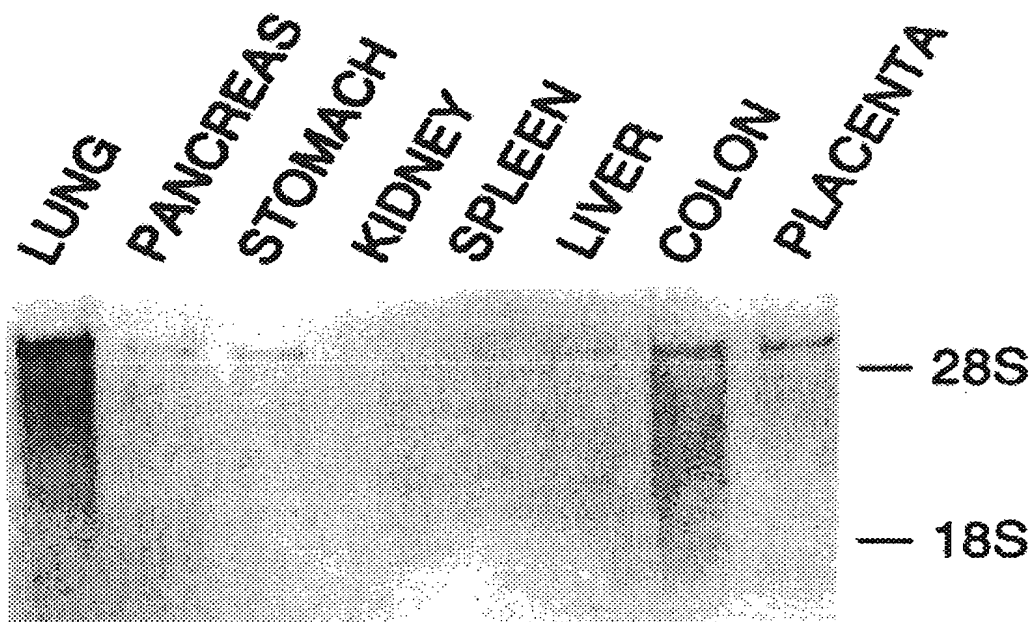


FIG. 17

REPLACEMENT SHEET

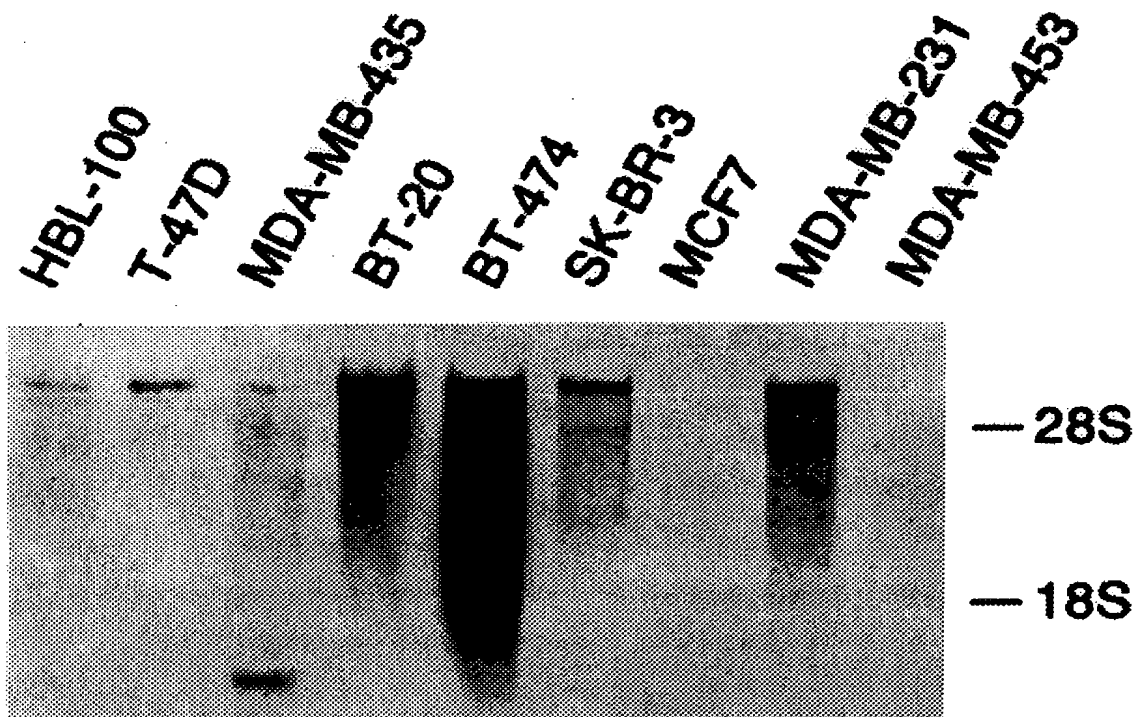


FIG. 18

REPLACEMENT SHEET

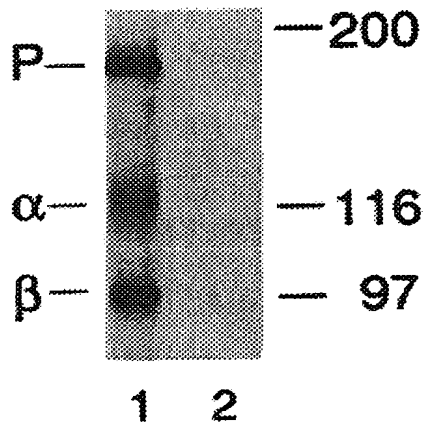


FIG. 19A

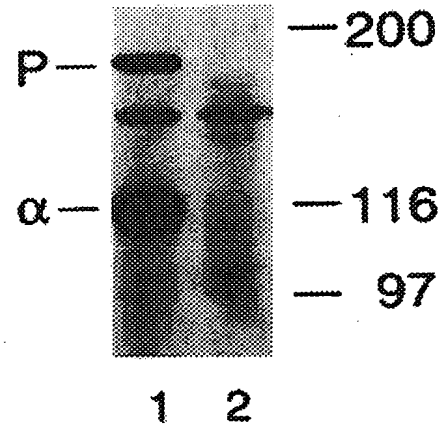


FIG. 19B

REPLACEMENT SHEET

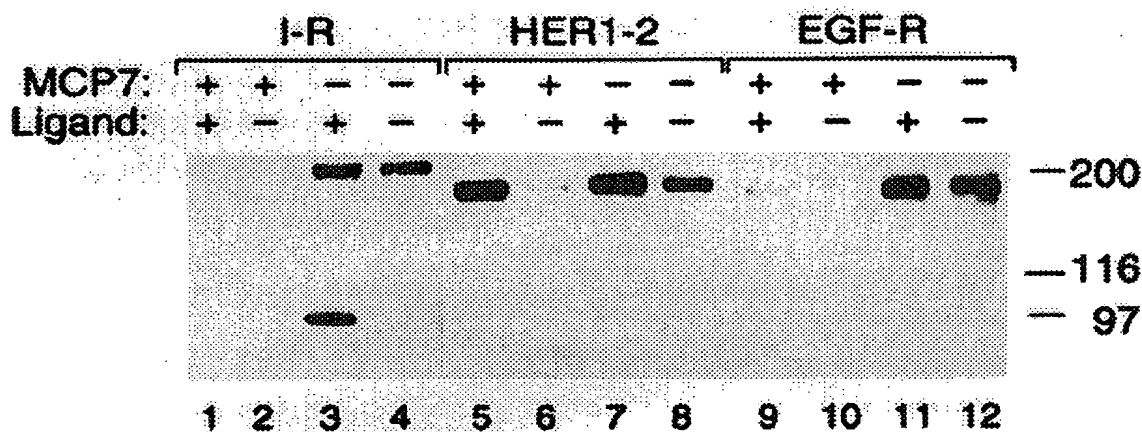


FIG. 20A

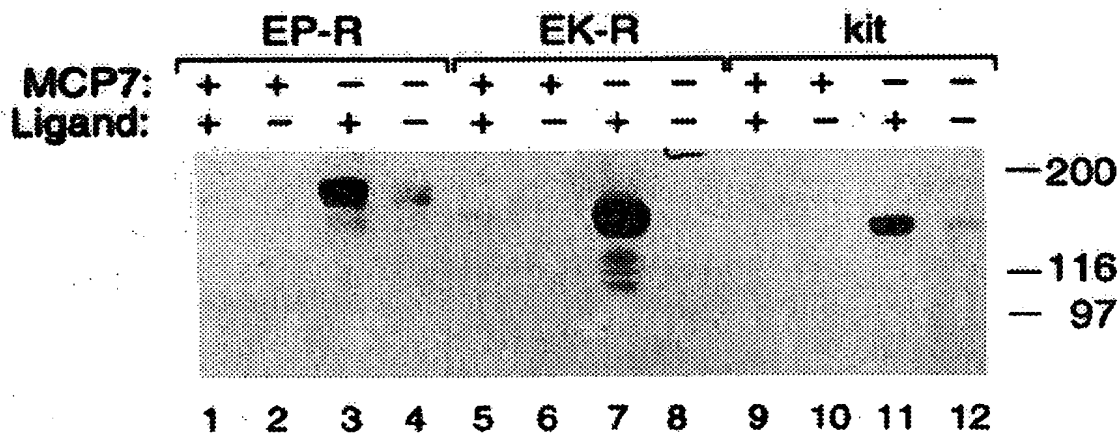


FIG. 20B

REPLACEMENT SHEET

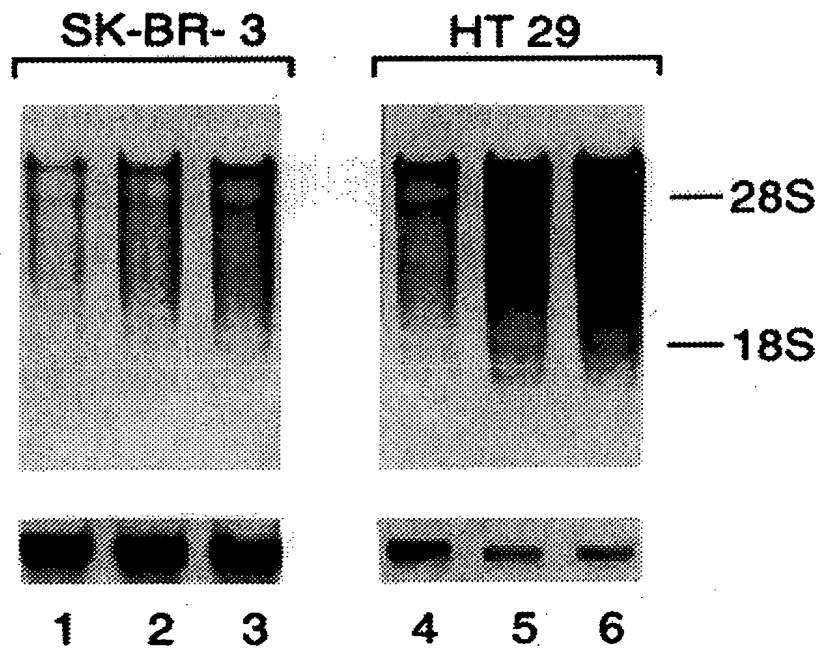


FIG. 21A

FIG. 21B

REPLACEMENT SHEET

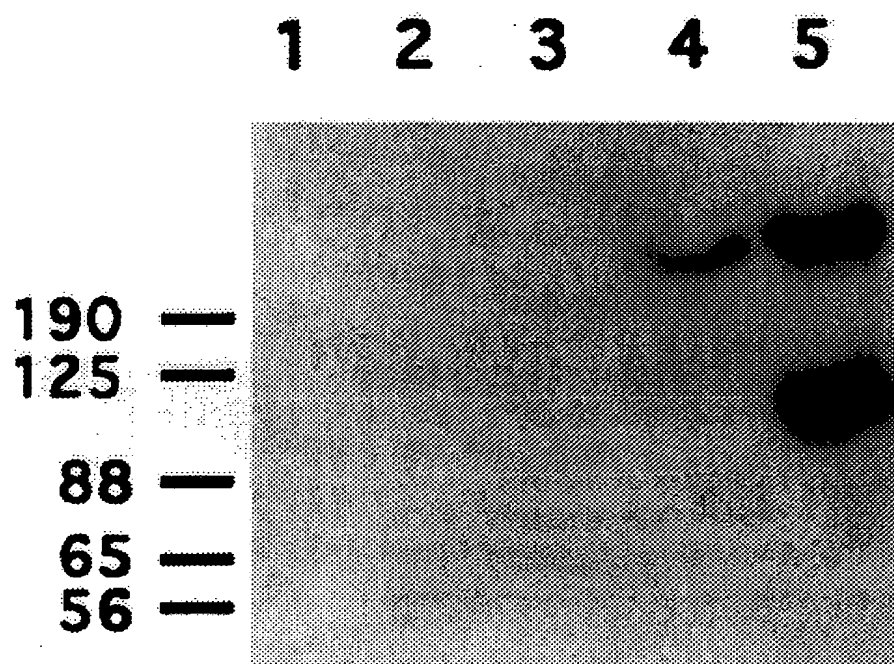


FIG. 22A

REPLACEMENT SHEET

CONTROL

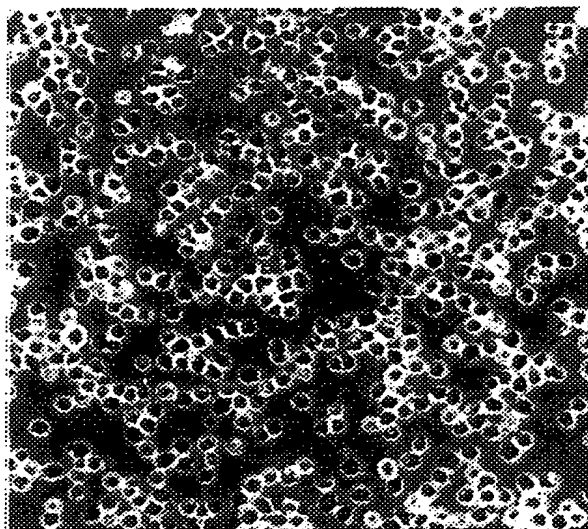


FIG. 22B

R-PTP-K

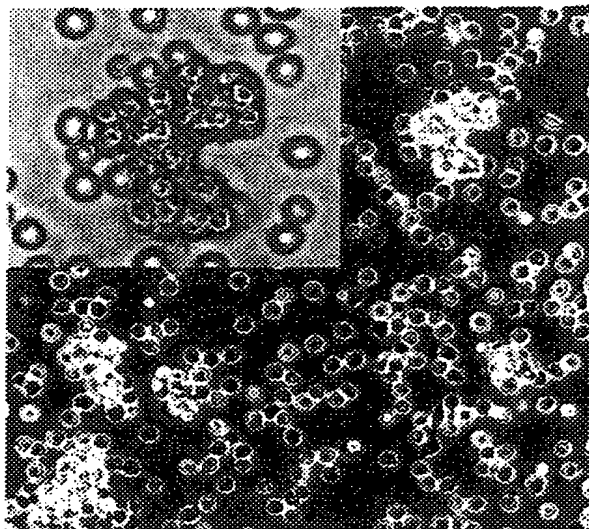


FIG. 22C

REPLACEMENT SHEET

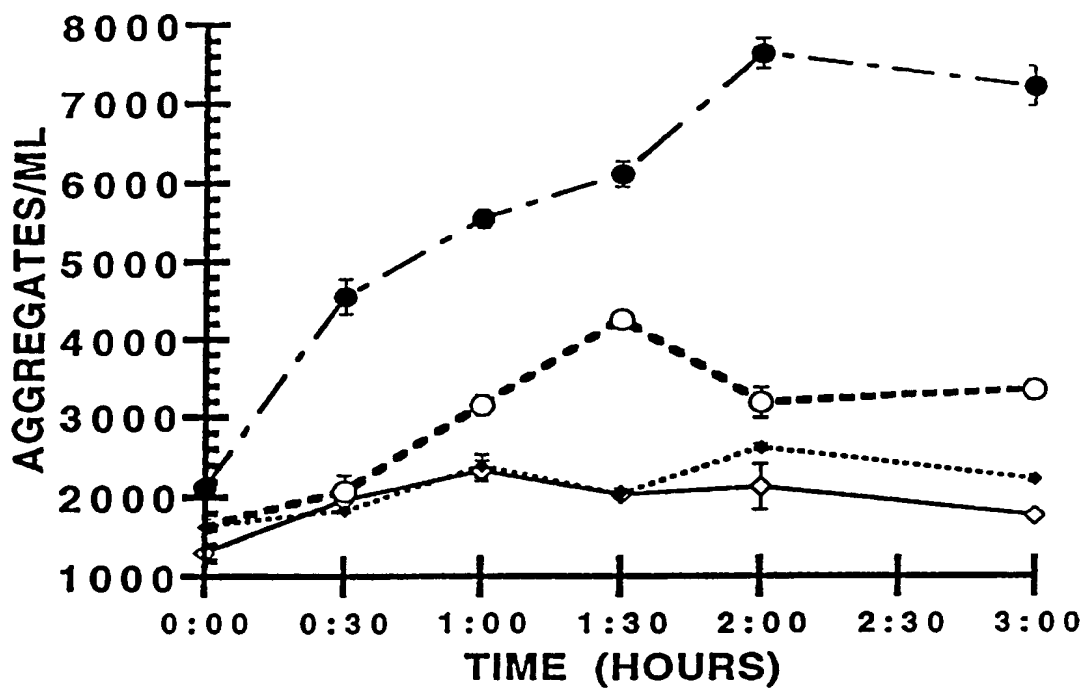


FIG. 22D

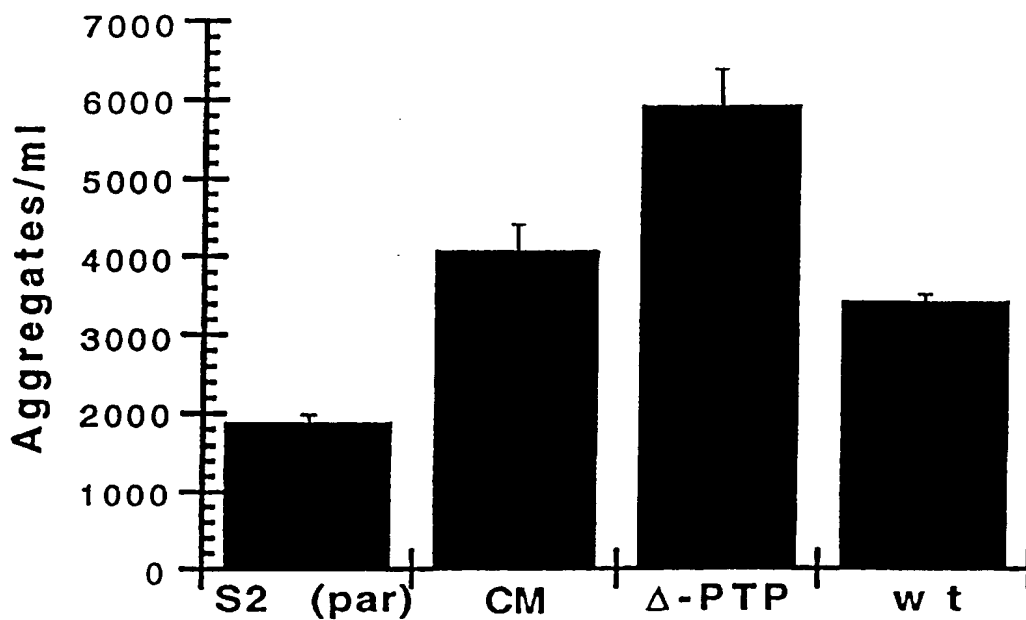


FIG. 22E

REPLACEMENT SHEET

$K^- (dil) + K^+$

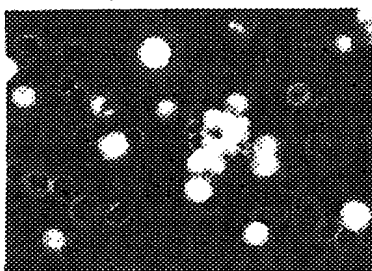


FIG. 23A

$K^- + K^+ (dil)$

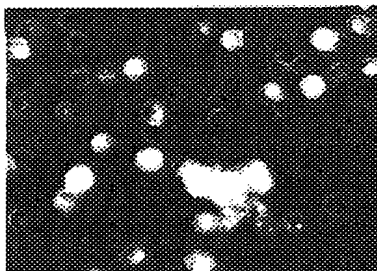


FIG. 23B

$K^+ + K^+ (dil)$

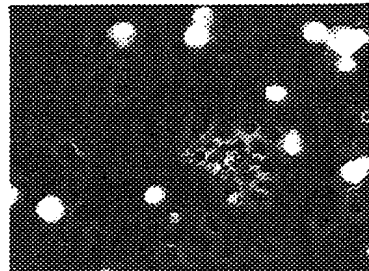


FIG. 23C

REPLACEMENT SHEET

FIG. 24A

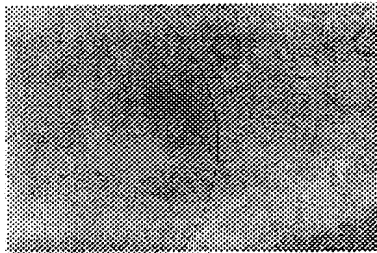


FIG. 24B

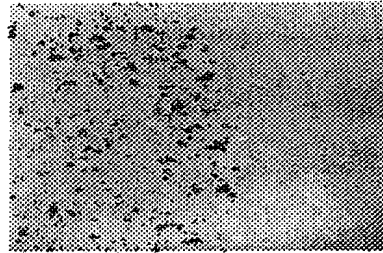
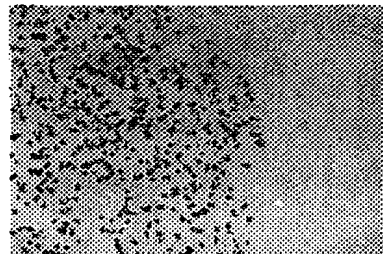


FIG. 24C



FIG. 24D



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